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Exo III Generated Structures

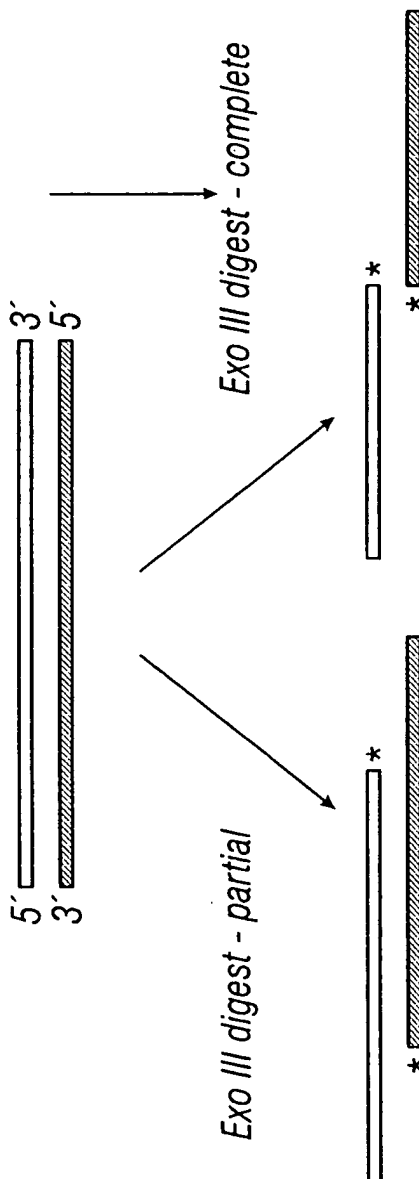


FIG. 1

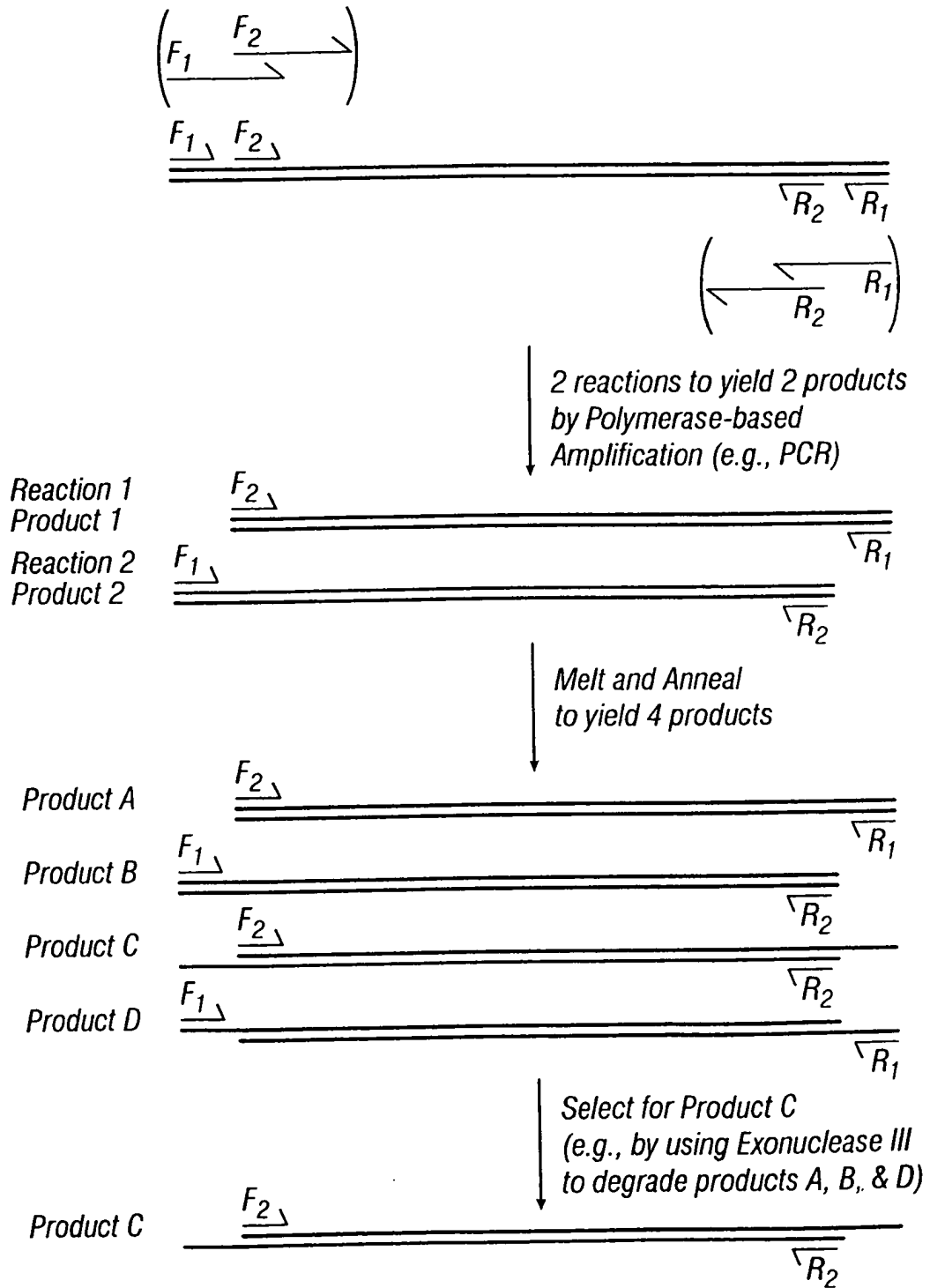
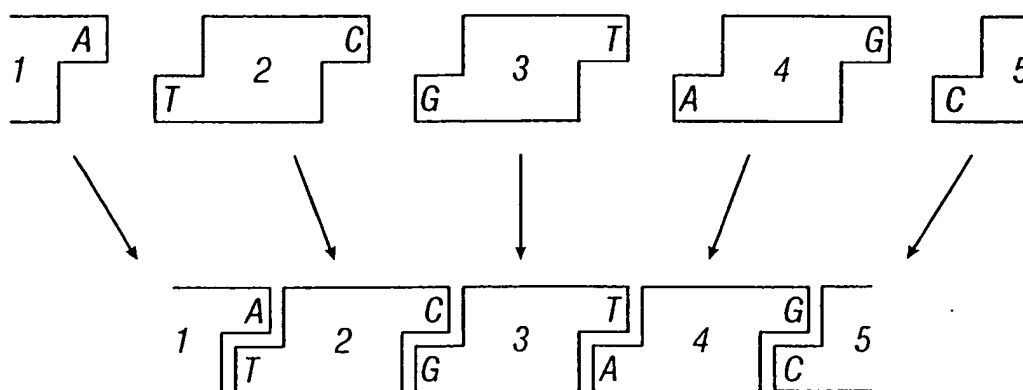
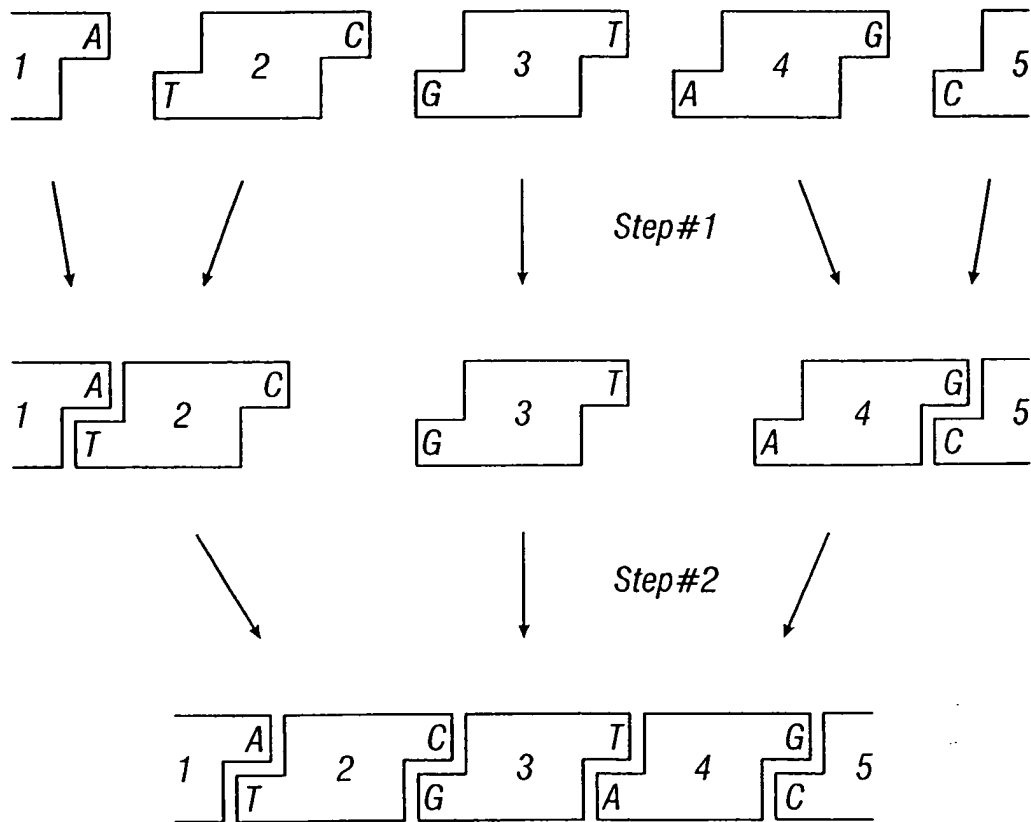


FIG. 2

*Panel A.**Panel B.**Panel C.**Panel D.***FIG. 3**

*Panel A.**Panel B.***FIG. 4A**

*Panel C.*



**FIG. 4B**

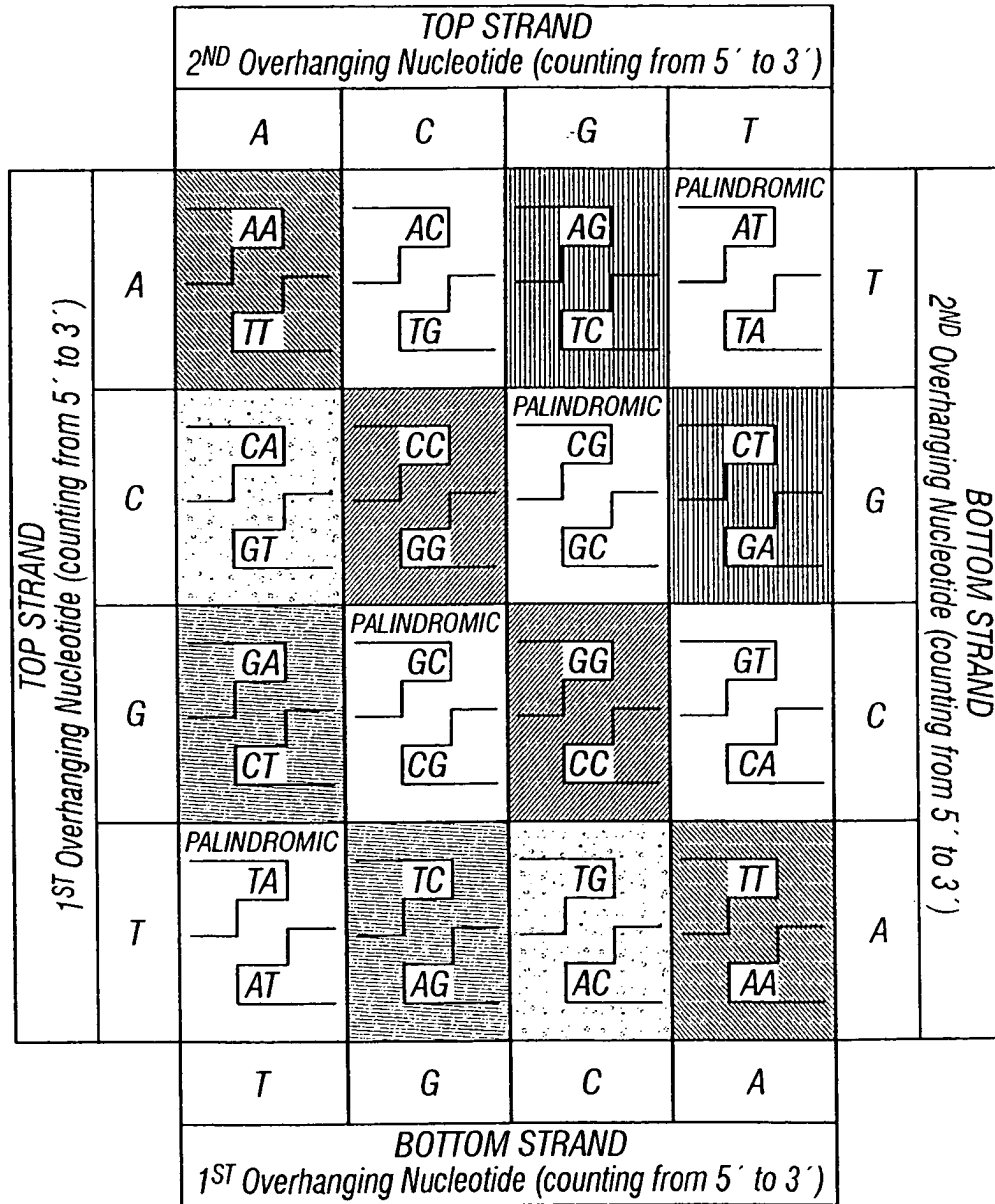
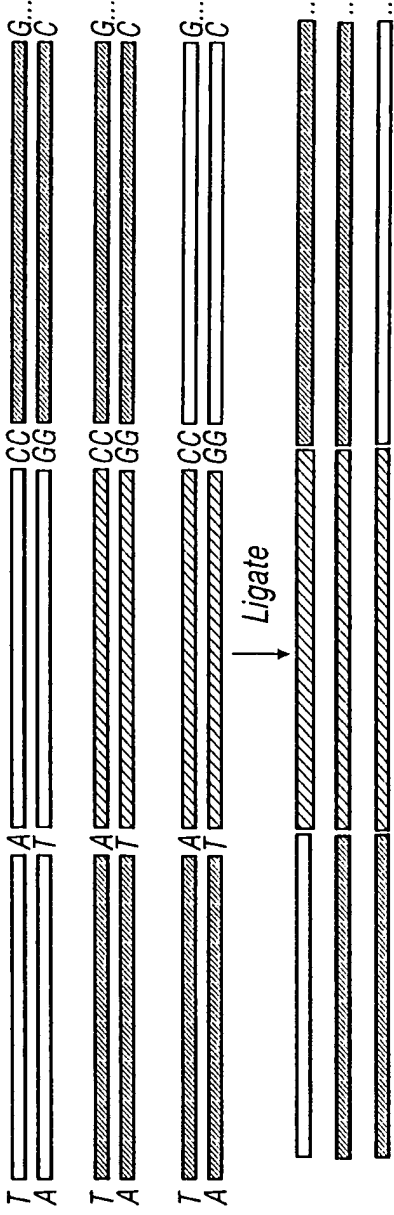


FIG. 5

Select for full length

[illegible]
$$8 + 8 + 8 + n = 144 \text{ d.s oligos}$$


$8^{18} = 2 \times 10^{16}$  Reassembled Gene Variants

**FIG. 6A**

100  
 ACACGGGCCA GGGTGATTCC GTTCTGTTTC TTCACGGCAA CCCGACGTCG  
 ACGTGGGAGA GGGGACCCG ATCGTGTTCC TCCACGGAAA TCCACGTCG  
 AGATGGGCGA GGGTGATCCC ATCATTTTCC AACACGGCAA TCCGACCTCA  
 ACGAAGGCAA GGGTGACGCC ATCGTCTTTC AGCACGGCAA CCCACGTCG  
 AAGTGGGACG GGGGACCCC ATCGTACTCT TGCACGGCAA CCCACCTCG  
 ATACCGGCCA GGGAGCGCCG ATCGTGTTCC TTCACGGCAA CCCGACTTCC  
 GCGTCGGCGA T...CTTCCC GTCGTGTTCC TGCACGGCAA CCCACGTCG  
 GACCGCGGGA TGGCACGCCT GTGCTGTTCC TGCACGGTAA CCCGACCTCG  
 -----G--- -----C- -T--T--T-- -CACGG-AA -CC-AC-TC-

FIG. 6B

Represents 15% of gene

150  
 TCGTATCTGT GGAGGGGCGT AATGCCCTTT GTGACGGACG TCGCCCGATG  
 TCGTACCTGT GCGGGAACGT GATCCCCAC GTTGCCGGCT TGGACGCTG  
 TCGTACCTGT GCGCAACAT CATGCCCAT GTGCAACAGC TGGTCGCTG  
 TCTTACTTGT GCGCAACAT CATGCCGCAC TTGGAAGGC TGGCCGGCT  
 TCGTACCTCT GCGCAACGT GTTGCCGCAC CTGGCCCGT TAGGCCGCTG  
 TCCTATCTTT GCGCAACAT CATCCCCAT CTCGCGGATC ACGCAGATG  
 TCTACGCTCT GCGCAACGT GATCCCCGCAC GTCGCTGGCC AGCACGGTG  
 TCCTACCTGT GCGCAACAT CATCCCCCAT GTAGCACCGA GTCATCGGTG  
 TC--A--T-T GG-G---C-T --T-CC---- -T-----G---

FIG. 6C



NcoI  
150am13\_00 cATGATGCACG GCGATATTTC ATCGAGCAAT GACACGGTCG GCGTTGCCGT CCGT  
150AM7\_001 cATGCATCACG GCGACATTTC ATCGAGCAAT GACACGGTCG GCGTTGCCGT CCGT  
431am7\_002 cATGAGACACG GAGATATCTC CAGCAGCAAC GATTGCGTGG GCGTGGCCGT CCGT  
GAG GT  
150am13\_00 CGTGAACCTAC AAGATGCCCTC GCCTTCATAC CAAGGCGGAG GTTTAGCGA  
150AM7\_001 CGTGAACCTAC AAGATGCCGC GGCTTCACAC CAAGGCTGAG GTGCTGGCCA  
431am7\_002 CGTGAACCTAC AAGATGCCGC GGCTGCATAC CCGCGCGGAG GTGATGGAGA  
CGG  
150am13\_00 ACGCCAGAA GATCGGCGAG ATGATCGTCG GCATGAAGAC CCGCCTGCCG  
150AM7\_001 ACTGCCGCAA GATCGCCGAC ATGCTGGTCG GCATGAAGAG CCGCCTGCCG  
431am7\_002 ACGCCCGCAA GATCGCCGAC ATGGTCGTGG GCATGAAGCG CCGCCTGCCG  
CCACG  
150am13\_00 GGAATGGATC TGGTGATCTT CCCGGAATAT TCGACCCACG GCATCATGTA  
150AM7\_001 GGAATGGATC TGGTGATCTT CCCGGAATAT TCCACCCACG GCATCATGTA  
431am7\_002 GGCATGGACC TGGTCATCTT CCCCAGGTAC TCCACCCACG GCATCATGTA  
CCC GG  
150am13\_00 CGACTCCAAG GAAATGTACG ATACCGCGTC CGTCGTGCCG GGCAGGAGA  
150AM7\_001 CGACTCCAAG GAGATGTACG ACACGGCGTC GACGGTGCCG GGTGAAGAGA  
431am7\_002 CGACGCCAAG GAAATGTACG AAACCGCTTC GGCCATTCCG GGCAGGAGA  
G GGG  
150am13\_00 CCGAGATTTT TGCCGAAGCC TGCCGCAAGG CGAAAGTCTG GGGCGTGTTT  
150AM7\_001 CCGAGATTTT CGCCGAGGCC TGCCGCAAGG CCAAGGTCTG GGGCGTGTTT  
431am7\_002 CTGCTGTGTT CGCCGACGCC TGCCGCAAGG CCAACGTATG GGGCGTGTTT

FIG. 7A

150am13_00	TCGCTCACCG	GCGAACGTCA	CGAGGAACAT	CCGAAG	AAAG C	AAGG	CGCCCTACAA
150AM7_001	TCGCTGACCG	GCGAGCGCCA	CGAGGAGCAT	CCCAATAAAG			CGCCGTACAA
431am7_002	TCGCTGACGG	GCGAGCGCCA	CGAAGAGCAC	CCGAACAAGG			CGCCGTACAA
150am13_00	CACGCTGATC	CTGATGAACG	ACAAGGGCGA	GGTGGTCC	CAG AA		AAATACCGCA
150AM7_001	CACCCTGATC	CTGATGAACG	ACAAGGGTGA	AGTCGTT			AAATATCGCA
431am7_002	CACGCTCATC	CTGATGAACA	ACAAGGGCGA	GATCGTGCAG			AAATACCGCA
150am13_00	AGATCATGCC	GTGGGTTCGG	ATCGAGGGCT	GGTA			CAACTGCACC
150AM7_001	AGATCATGCC	GTGGGTGCCG	ATCGAAGGCT	GGTATCCCCG			CAACTGCACG
431am7_002	AGATCATGCC	CTGGGTGCCG	ATCGAAGGCT	GGTATCCCCG			CGATTGCACC
150am13_00	TACGTCTCCG	ACGGGCCCGAA	GGGCATGAAG	GTTCGCTGA			TCATCTGCCA
150AM7_001	TACGTCTCCG	AAGGCCCGAA	GGGCATGAAG	ATGTCGCTGA			TCATCTGCCA
431am7_002	TATGTGTCCG	AAGGCCCGCAA	GGGACTGAAG	ATCAGCCTCA			TCATCTGCCA
150am13_00	TGACGGCAAC	TATCCGGAAA	TCTGGCGCGA	CTGCGCCCATG			AAGGGCGCCG
150AM7_001	CGACGGCAAC	TACCCGGAAA	TCTGGCGTGA	CTGCGCGATG			AAGGGCGCCG
431am7_002	CGACGGCAAT	TACCCCGAGA	TCTGGCGCGA	TTGCGCCCATG			CGCGGCGCCG
150am13_00	AGCTGATCGT	GCGCTGCCAG	GGCTACATGT	ATCCGGCCAA			GGACAGCAG
150AM7_001	AACTGATCAT	CCGCTGCCAG	GGCTACATGT	ATCCCGCCAA			GGATCAGCAG
431am7_002	AGCTGATCGT	GCGTTGCCAG	GGATACATGT	ACCCGGCCAA			GGACAGCAG

FIG. 7B

150am13_00	GC	GTCATCATGG	CGAAGGC	GAT	GGCGTGGCG	AATAATTGT	ACGTCGCGGT
150AM7_001		GTGCTGATGG	CGAAAGCAAT		GGCCTGGCC	AACAACGTTT	ATGTCGCGGT
431am7_002		GTCATGGTGT	CCAAGGCCAT		GGCGTGGATG	AACAACGTCT	ACGTGGCGGT
			GGGCTTCG				
150am13_00		TTCCAATGCC	GGGGCTTCG		ATGGCGTCTA	TTCGTATTTC	GGCCACTCGG
150AM7_001		CGCCAATGCC	TCGGGCTTCG		ACGGCGTCTA	CTCGTATTTC	GGCCATTCGG
431am7_002		GGCCAATGCC	GGGGCTTCG		ACGGCGTGTA	TTCCTACTTC	GGCCATTCGG
			TTCGA				
150am13_00		CGATCATCGG	CTTCGATGGC		CGCACGCTCG	CGGAATGCGG	CGAGGAAGAA
150AM7_001		CGATCATCGG	CTTCGACGGC		CGTACCCCTCG	CGGAATGCGG	CGAGGAGGAT
431am7_002		CCATCATCGG	CTTCGACGGC		CGCACGCTGG	CGGAATGCGG	TGAAGAAGAC
			C AGTA				
150am13_00		TACGGCATCC	AGTATGCCCA		GCTTTCGAAG	ATGCTGATCC	GGACGCCCG
150AM7_001		TATGGCATCC	AGTATGCCGC		CATCTCCAAG	TCGCTGATCC	GGACGCCCG
431am7_002		ATGGCGGTGC	AGTACGCCCA		GCTCTCCACC	AGCCTGATCC	GGACGCCCG
			CAATC				
150am13_00		CCGCACCCGA	CAATCGGAAA		ACCATCTCTT	CAAGCTGGTG	CATCGTGGCT
150AM7_001		CCGCACCCGC	CAATCGGAAA		ACCATCTCTT	CAAGCTGGTG	CACCGTGGCT
431am7_002		CAAGAACATG	CAGTCGCAGA		ACCACTTGT	CAAGCTGGTG	CACCGCGGCT
			GATCAA				
150am13_00		ACACCGGGTT	GATCAACTCC		GGCGAGGGCG	ACCGCGGTCT	CGCGGCTGT
150AM7_001		ACACCGGCAT	GATCAATTCC		GGCGAGGGCG	ACCGCGGTGT	CGCGGCTTGC
431am7_002		ACACCGGCAA	GATCAATTCC		GGCGAAGAGG	CCACCGGCGT	CGCGGCATGC

FIG. 7C

150am13_00	TTA CCTTATGAGT	TCTACAACAA	ATGGATCGCC	GATCCGGAAG	GCACCCGCCGA
150AM7_001	CCGTATGATT	TCTATTGAA	ATGGATCGCC	GATCCCGAGG	GTACACGCCGA
431am7_002	CCGTACAACT	TCTACGCCAA	CTGGATCAAC	GATCCGGAGG	GCACGCGCAA
	ATGGT				
150am13_00	AATGGTCGAG	TCCTTTACCC	GGCCGACGGT	GGGAACCGAT	GAAGCGCCCCA
150AM7_001	GATGGTGGAA	TCCTTCACGC	GTCCGACGGT	GGGTGTGGAG	GAATGCCCGCA
431am7_002	GATGGTCGAA	TCCTTCACCC	GGTCCACCGT	GGGCACGCCG	GAGTGCCCCCA
	TCGAG				
150am13_00	TCGAAAGGCAT	CCCGAACAAAG	GTCGCGGTGC	ACCGCTGA	aagct
150AM7_001	TCGAGGGCAT	TCCGAACAAG	GCCACCACGC	ACCGCTGA	aagct
431am7_002	TGGACGGCAT	CCCCAACGAG	GACGCCAAGC	ACCGCTAG	aagct
					HindIII

FIG. 7D





FIG. 9

Gap Ligation

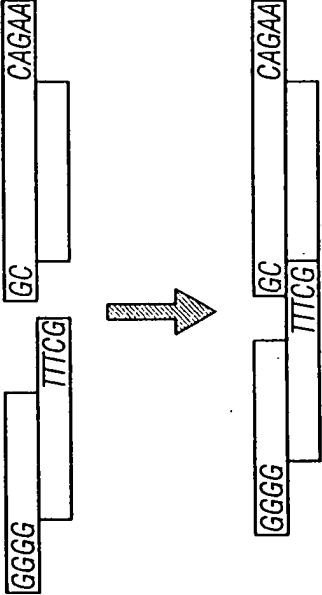


FIG. 10

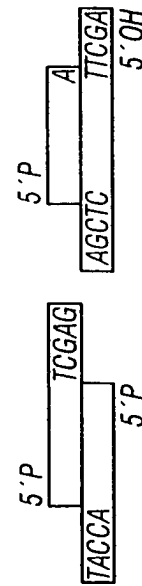
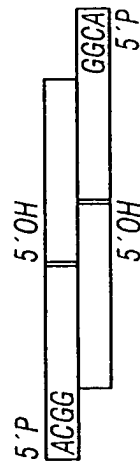
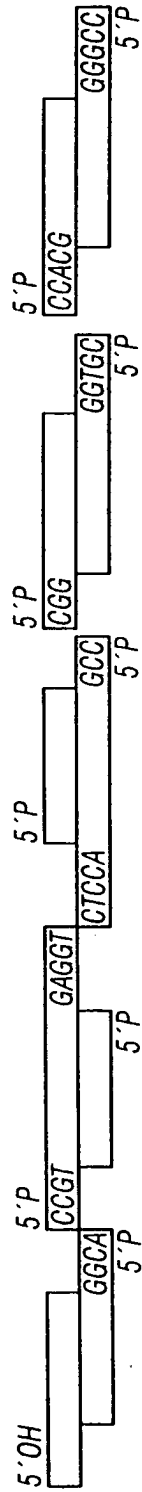


FIG. 11

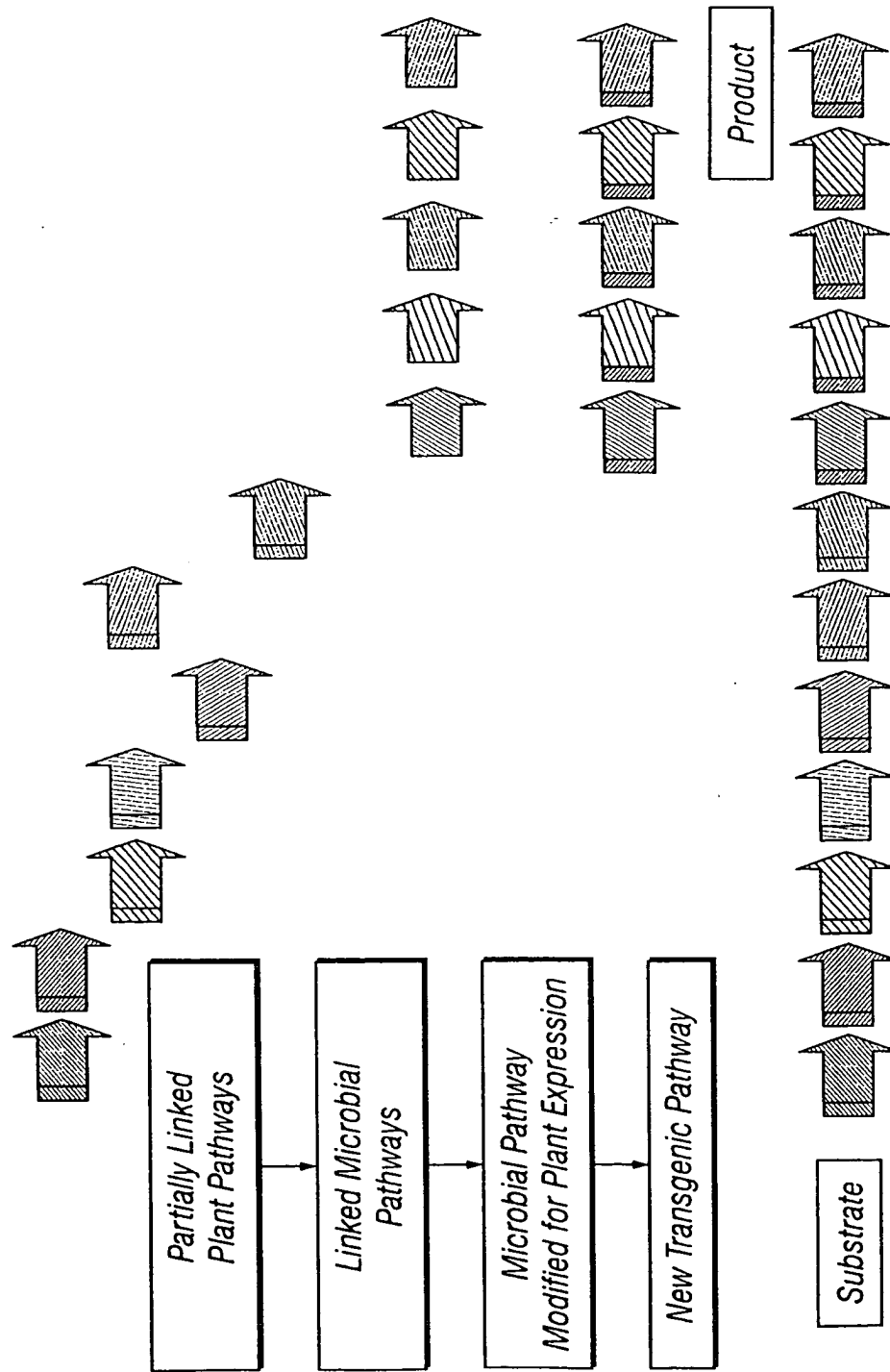
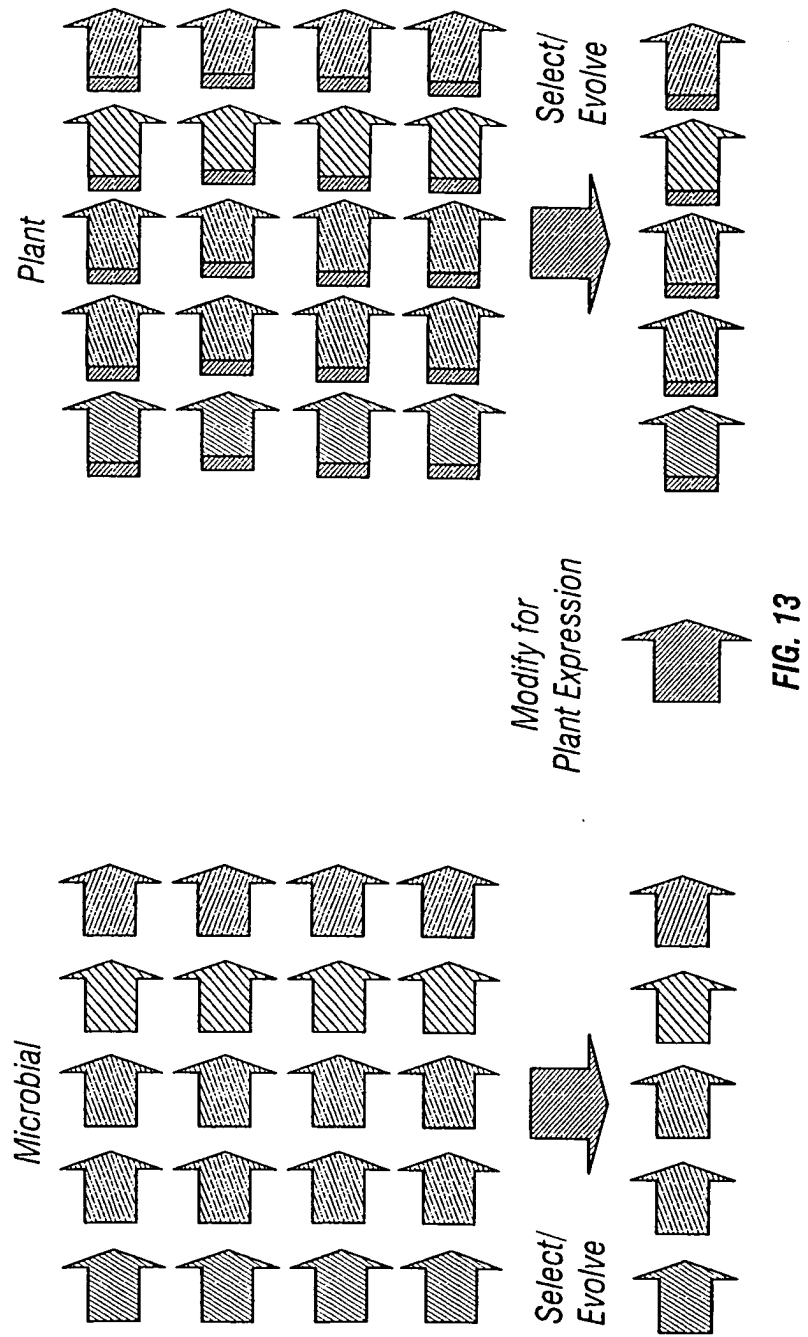


FIG. 12





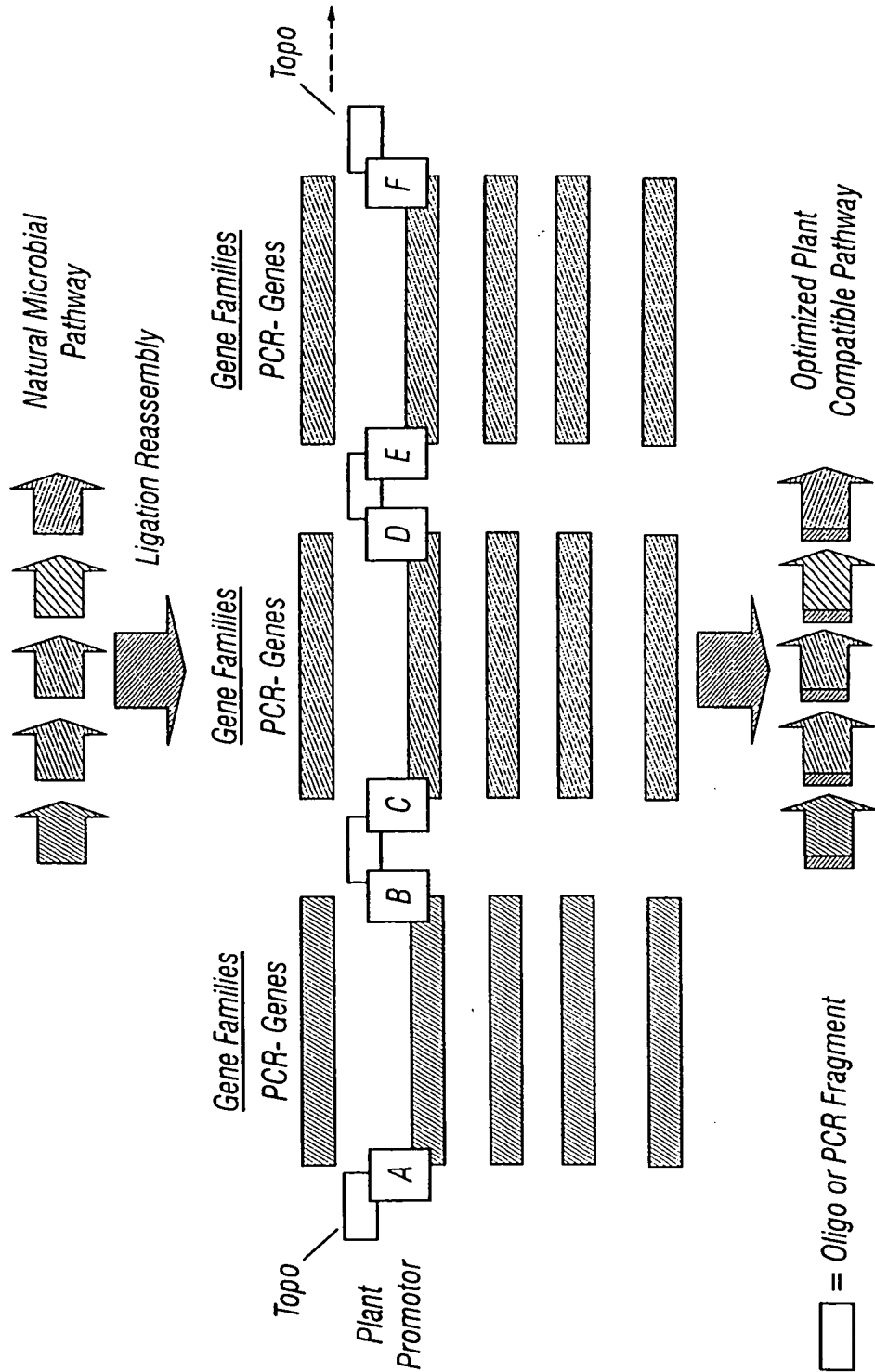
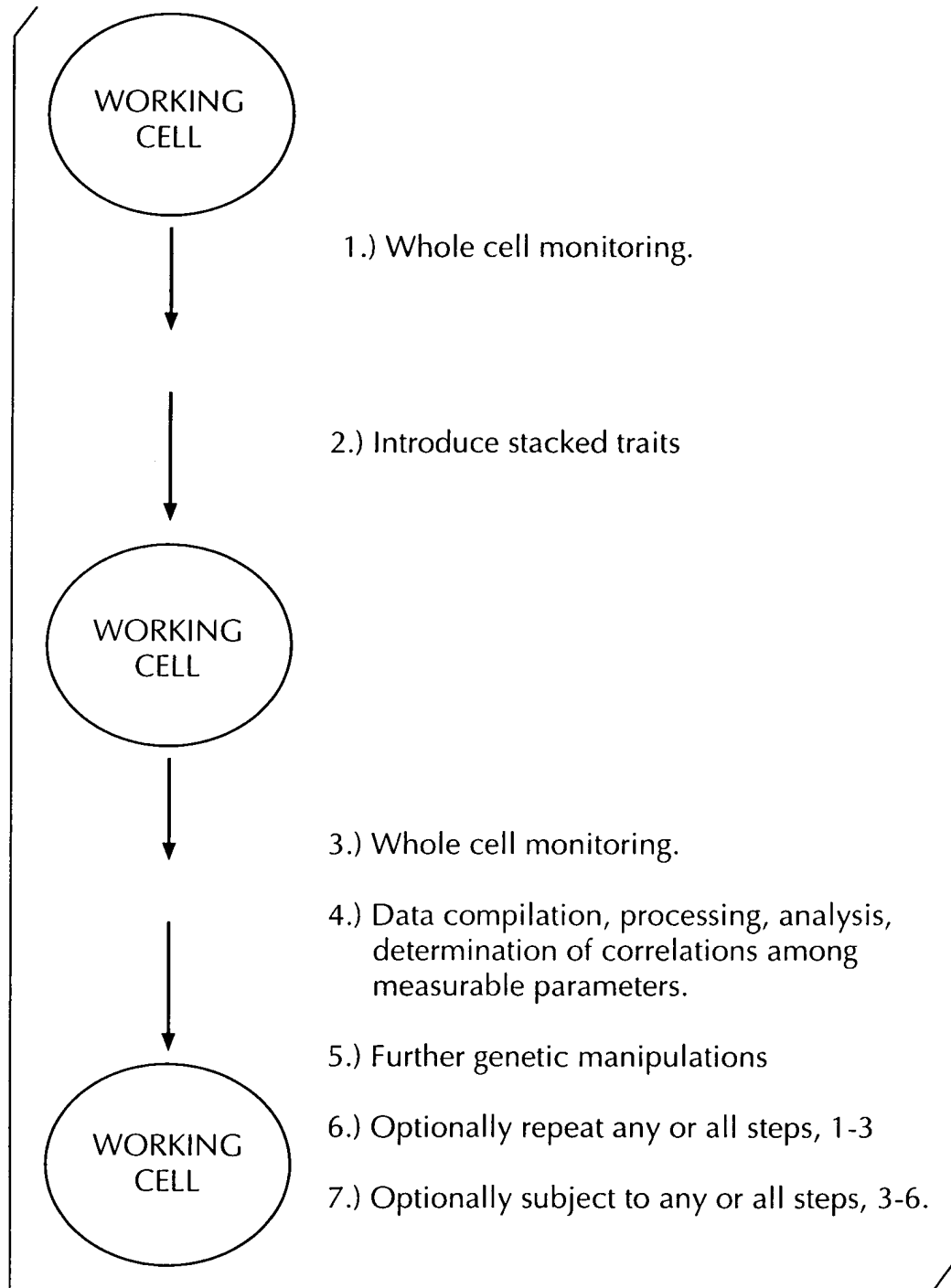
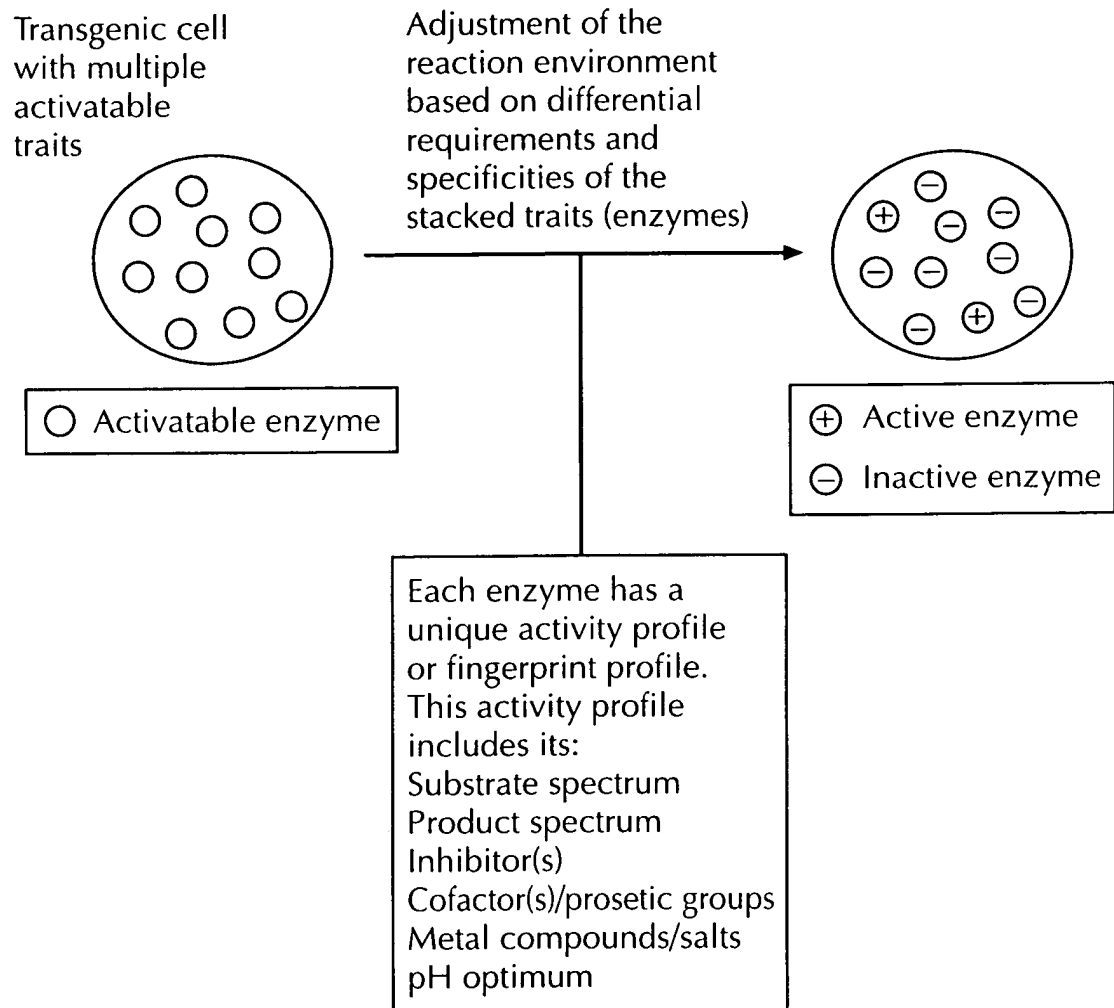


FIG. 14

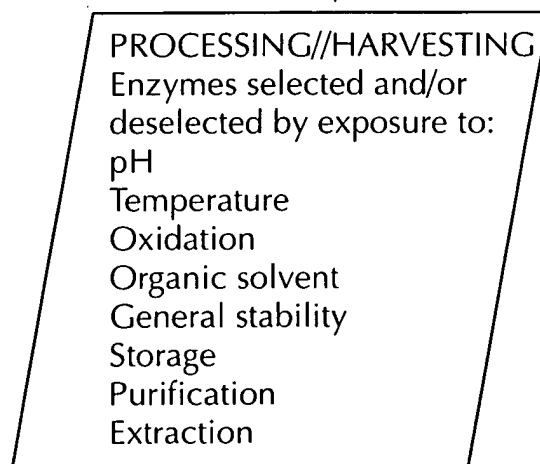
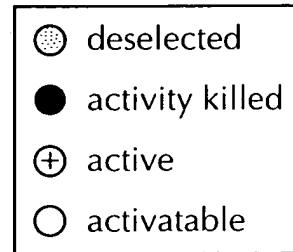
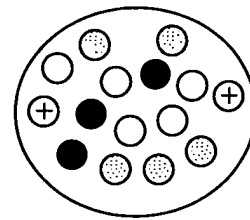
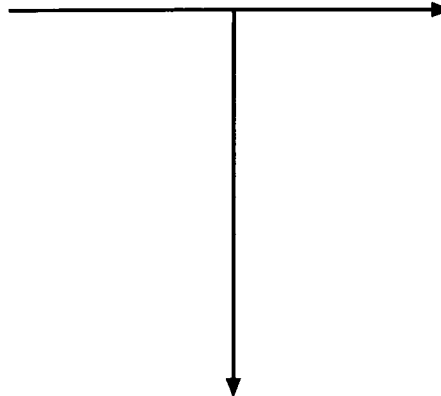
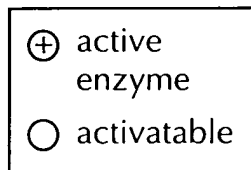
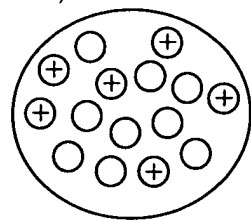
**FIG. 15**

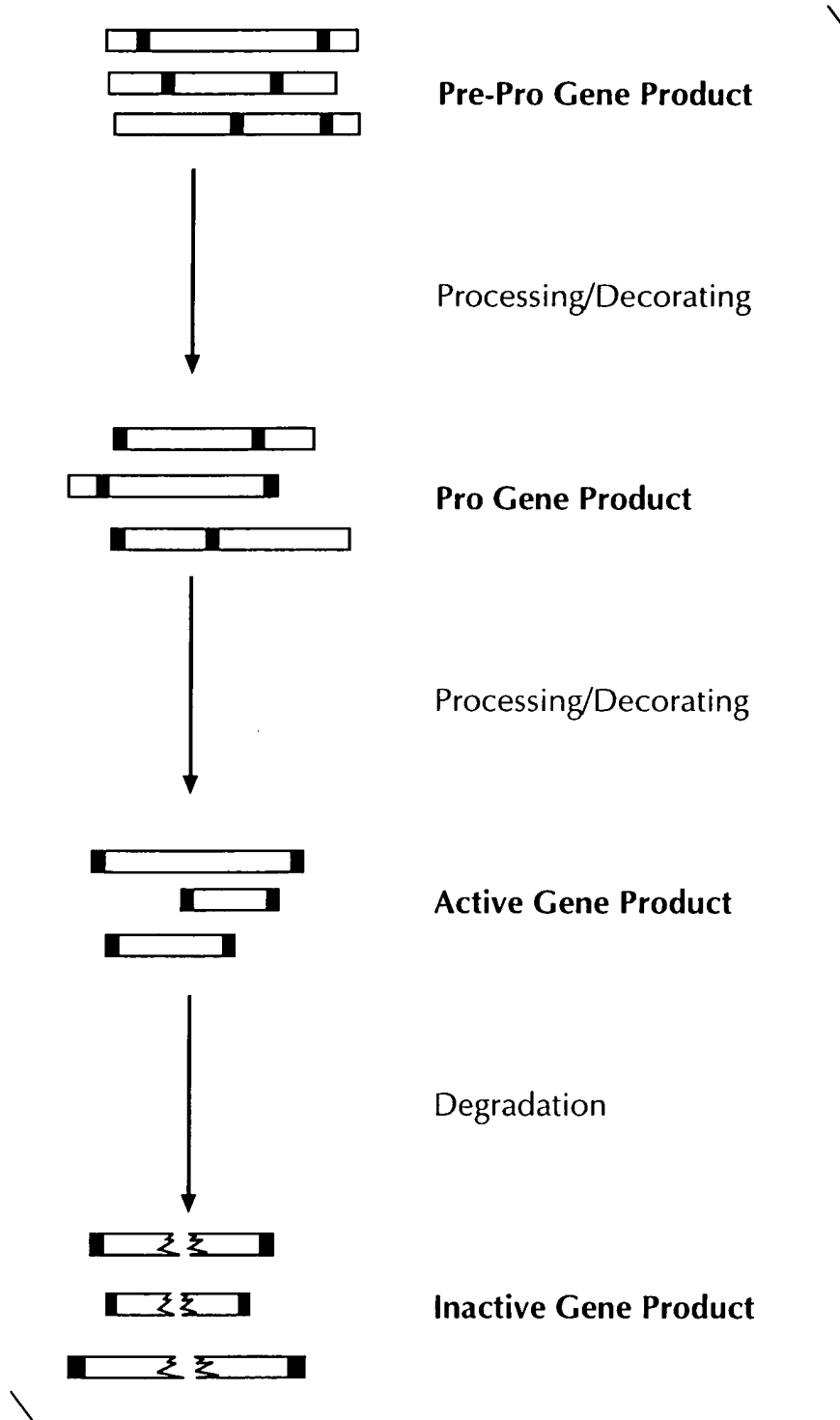


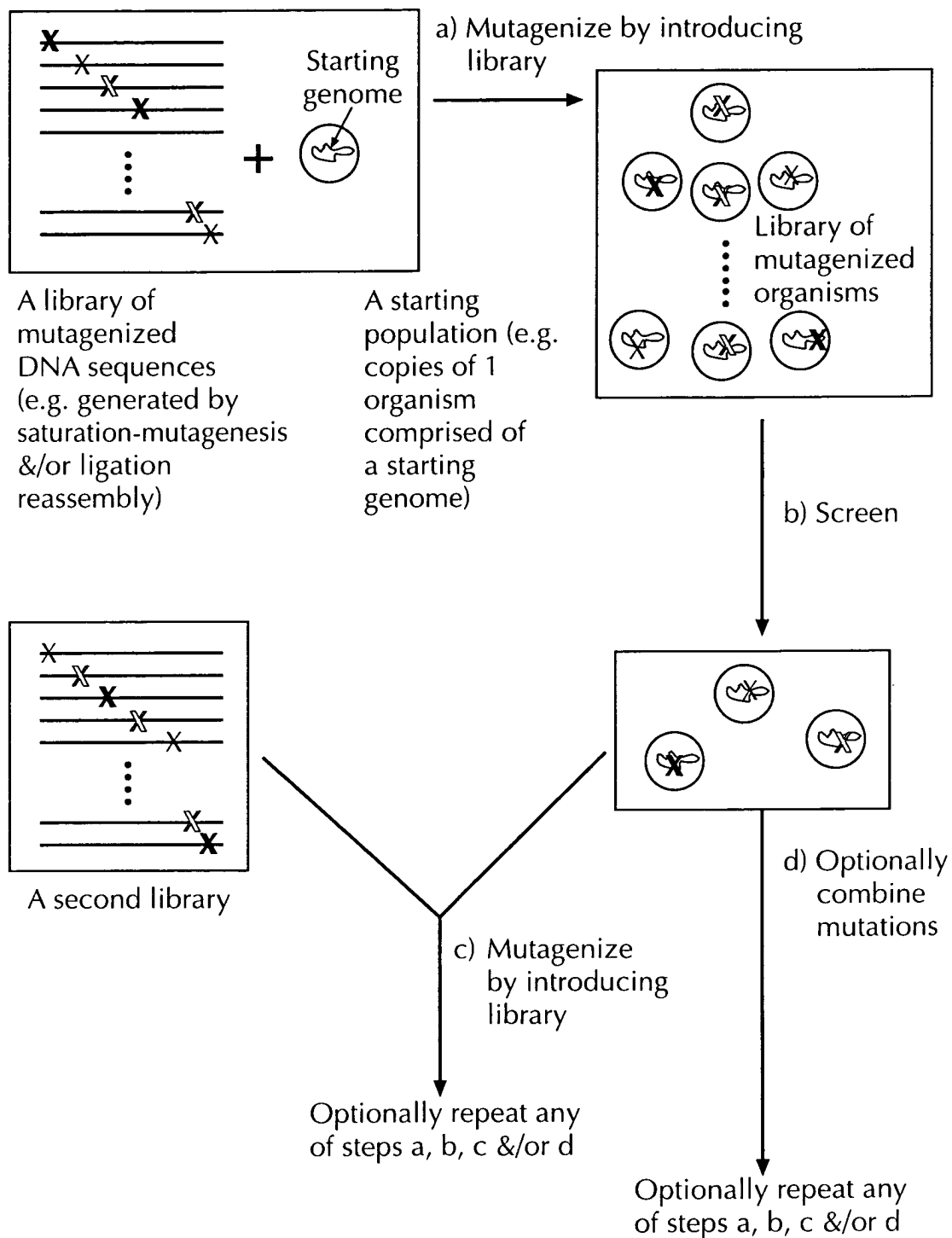
**FIG. 16**

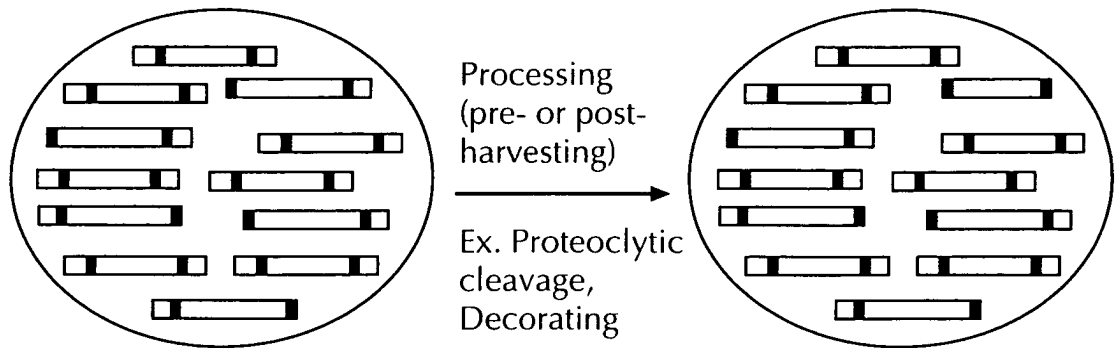
**FIG. 17**

Transgenic cell  
with multiple  
activatable  
traits,



**FIG. 18**

**FIG. 19**

**FIG. 20**

Inactive precursor gene products (ex. pre-pro hormones, pro-hormones pre-pro proteins, or pro-proteins).

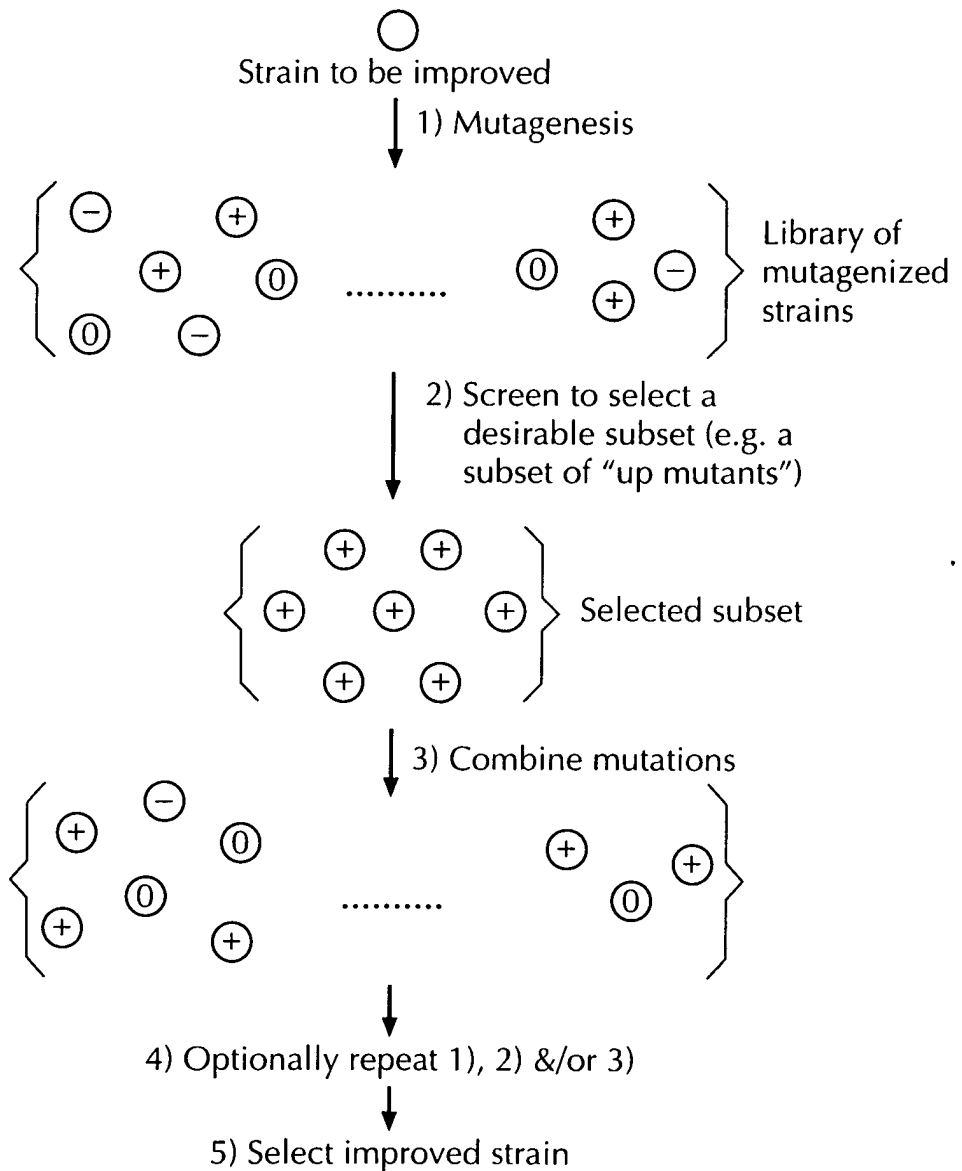
LEGEND:

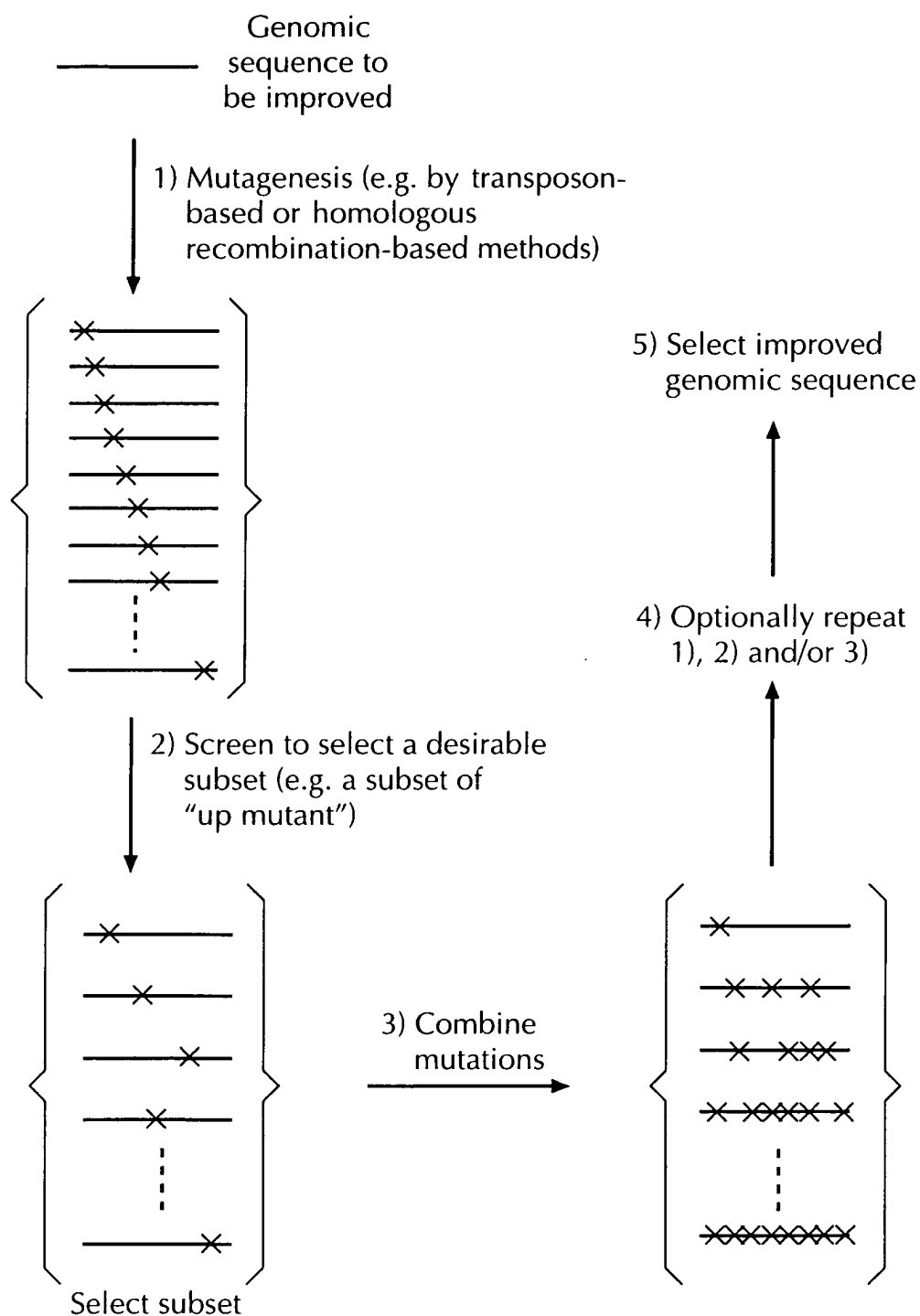
	pre-pro
	pro
	active



**FIG. 21**

- ⊕: Represents strains improved in one or more ways e.g. "up mutants"
- ⊖: Represents strains with adverse mutations e.g. "down mutants"
- : Represents strains with no improvement e.g. "null mutants"



**FIG. 22**

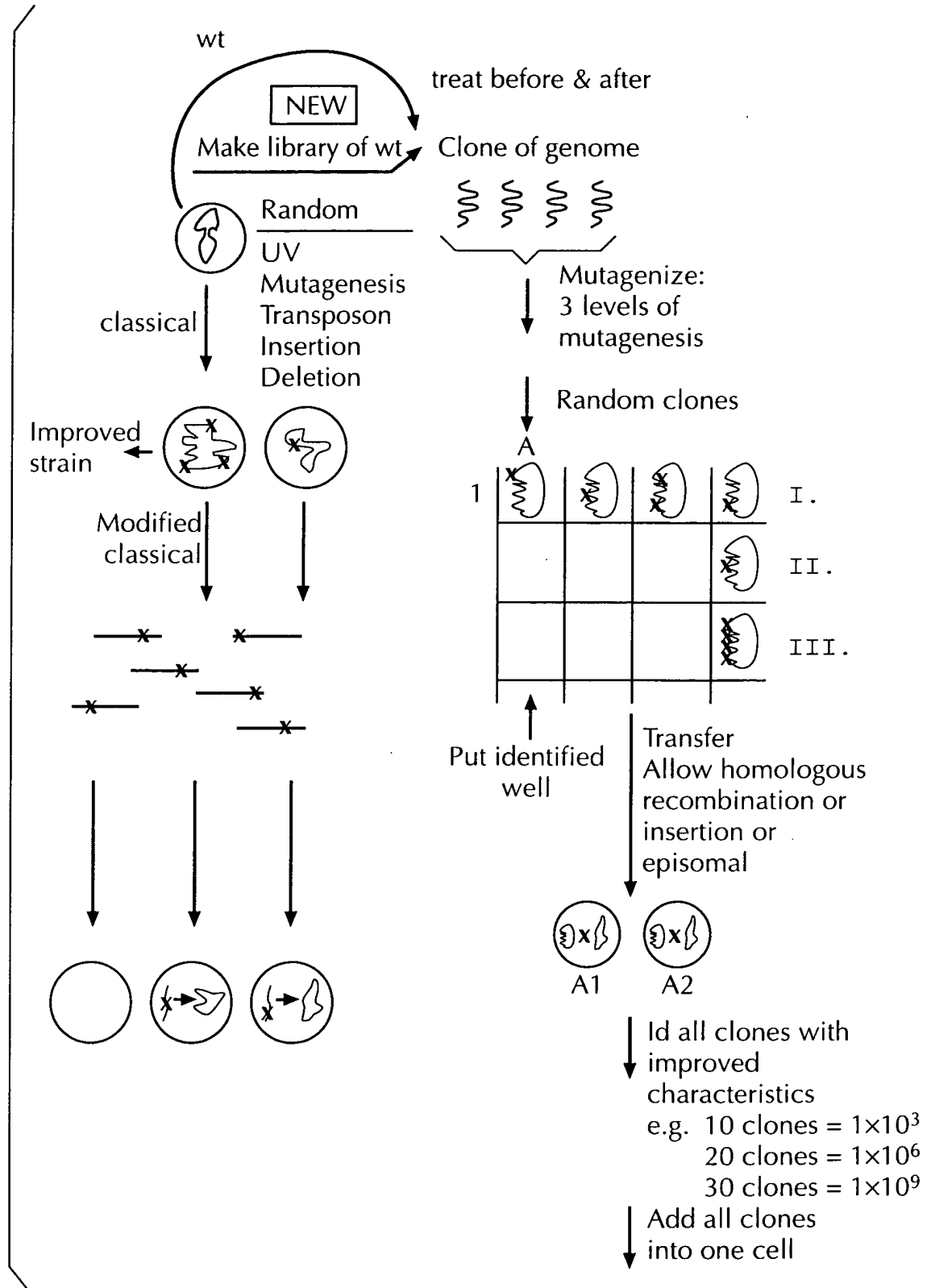
**FIG. 23**

FIG. 24

